

## WHAT IS CLAIMED IS:

1. A method of determining a base sequence for nucleic acid, electrophoresing a fragment sample of nucleic acid and determining the base  
5 sequence of the nucleic acid on the basis of detected data, comprising steps of:

(A) performing waveform shaping by Fourier transformation on data of a certain number  $N$  of points from the head of the detected data with a parameter of a previously set peak interval;

10 (B) determining the base sequence as to data of  $P$  points ( $P < N$ ) from the head of the data of  $N$  points;

(C) obtaining a peak interval from the result of the sequence determination;

15 (D) performing waveform shaping by Fourier transformation on data of  $N$  points from a position returning by  $L$  points ( $L < M$ ) from final data precedently subjected to the sequence determination with a parameter of a precedently obtained peak interval; and

20 (E) determining the base sequence as to data of  $M$  points ( $M < N$ ) of a central portion to be connected with data precedently subjected to the sequence determination among data of  $N$  points subjected to second or later waveform shaping, wherein

the steps (E)  $\rightarrow$  (C)  $\rightarrow$  (D) are repeated until data disappear or no analysis is required despite presence of data.

25 2. The method of determining a base sequence for nucleic acid according to claim 1, wherein

FFT treatment is applied as the waveform shaping by Fourier transformation.

30 3. The method of determining a base sequence for nucleic acid

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